

## SEQUENCE LISTING

<110> Ziv , Shani

Shoseyov, Oded

<120> PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND RECOMBINANT  
PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSUES OR CULTURED PLANT CELLS

<130> 01/22924

<160> 26

<170> PatentIn version 3.1

<210> 1

<211> 4

<212> PRT

<213> Unknown

<220>

<223> ER retaining signal peptide

<400> 1

His Asp Glu Leu

1

<210> 2

<211> 4

<212> PRT

<213> Unknown

<220>

<223> ER retaining signal peptide

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Lys Asp Glu Leu

1

<210> 3

<211> 150

<212> DNA

<213> *Arabidopsis thaliana*

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<211> 29

<212> DNA

<213> Artificial sequence

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<223> Single strand DNA oligonucleotide

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<211> 28

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<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

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<211> 1305

<212> DNA

<213> Artificial sequence

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<223> ProtL-CBDcex DNA construct

<400> 6  
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 aagacaatgg agaataact gtagatgttg cagataaagg ttatacttta aatattaaat 240  
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<211> 32

<212> DNA

<213> Artificial sequence

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<223> Single strand DNA oligonucleotide

<400> 7

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<210> 8

<211> 43

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

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aaaagtcgac ttaaagttca tcatgctcga cgccgaccgt gca 43

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 <213> Artificial sequence

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<223> Single strand DNA oligonucleotide

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<210> 10

<211> 43

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

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<210> 11

<211> 1418

<212> DNA

<213> Artificial sequence

<220>

<223> pUC19-cell-ProtL-cexNG-HDEL fusion construct

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 tggcggcggt agaaaaataa gaagaaacac cagaaacacc agaaactgat tcagaagaag 180  
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 aaggaacatt tgaaaaagca acatcagaag cttatgagta tgcagatact ttgaagaaag 300  
 acaatggaga atatactgta gatgttgtag ataaagggtta tacttttaaat attaaatttg 360  
 ctggaaaaga aaaaacacca gaagaaccaa aagaagaagt tactattaaa gcaaacttaa 420  
 tctatgcaga tggaaaaaca caaacagcag aattcaaagg aacatttgaa gaagcaacag 480  
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 aacaaaaaga agaagttact attaaagcaa acttaatcta tgcagatgga aaaacacaaa 660  
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<211> 467

<212> PRT

<213> Artificial sequence

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<223> pUC19-cell1-ProtL-cexNG-HDEL fusion encoded product

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 20 25 30

Leu Arg Lys Ser Arg Met Ala Ala Val Glu Asn Lys Glu Glu Thr Pro  
 35 40 45

Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val Thr Ile Lys Ala Asn  
 50 55 60

Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala Glu Phe Lys Gly Thr  
 65 70 75 80

Phe Glu Lys Ala Thr Ser Glu Ala Tyr Glu Tyr Ala Asp Thr Leu Lys  
 85 90 95

Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr  
 100 105 110

Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys  
 115 120 125

Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr  
130 135 140

Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala  
145 150 155 160

Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val  
165 170 175

Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys  
180 185 190

Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn  
195 200 205

Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr  
210 215 220

Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala  
225 230 235 240

Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
245 250 255

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro  
260 265 270

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys  
275 280 285

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu  
290 295 300

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr  
305 310 315 320

Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly  
325 330 335

Lys Lys Val Asp Glu Lys Pro Glu Gly Ile Pro Pro Thr Pro Thr Pro  
340 345 350

Thr Ser Ala Ser Gly Pro Ala Gly Cys Gln Val Leu Trp Gly Val Asn  
355 360 365

Gln Trp Asn Thr Gly Phe Thr Ala Gln Val Thr Val Lys Asn Thr Gly  
370 375 380

Ser Ala Pro Val Asp Gly Trp Thr Leu Thr Phe Ser Phe Pro Ser Gly  
385 390 395 400

Gln Gln Val Thr Gln Ala Trp Ser Ser Thr Val Thr Gln Ser Gly Ser  
405 410 415

Ala Val Thr Val Arg Asn Ala Pro Trp Asn Gly Asn Ile Pro Ala Gly

420

425

430

Gly Thr Ala Gln Phe Gly Phe Gln Gly Ser His Thr Gly Thr Asn Ala  
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Ala Pro Thr Ala Phe Ser Leu Asn Gly Ala Pro Cys Thr Val Gly His  
 450 455 460

Asp Glu Leu  
 465

<210> 13

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 13  
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25

<210> 14

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 14  
 cttaaagttc atcatga

17

<210> 15

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 15  
 aaaaccggg atggcgcgaa aatc

24

<210> 16

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Single strand DNA oligonucleotide

<400> 16

aaaagacgtc ttacggagag cgtcgcggta atc

33

<210> 17

<211> 1560

<212> DNA

<213> Artificial sequence

<220>

<223> pBS-Sig-cex-Fx-HDEL fusion construct

<400> 17

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gaccttctct tttccctcgg gtcagcaggt aactcaggct tggatcatcta cagttacca	300
gtctggatcc gctgttacag ttcgtaacgc tccgtggaac ggtaatatc ctgcagggtg	360
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ccacgagaag ggccggcagt ccaccaggct caagatgctg gaggtgccct acgtggaccg	1260
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 gaagtacggg atctacacca aggtcaccgc cttctcaag tggatcgaca ggtccatgaa 1500  
 aaccaggggc ttgcccaagg ccaagcctac tagtcatgat gaactttaag agctccagct 1560

<210> 18

<211> 509

<212> PRT

<213> Artificial sequence

<220>

<223> pBS-Sig-cex-Fx-HDEL fusion encoded product

<400> 18

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Leu Phe Ser Pro Pro Ile Tyr Ser Ala Gly His Asp Tyr Arg Asp Ala  
 20 25 30

Leu Arg Lys Thr Ser Gly Pro Ala Gly Cys Gln Val Leu Trp Gly Val  
 35 40 45

Asn Gln Trp Asn Thr Gly Phe Thr Ala Gln Val Thr Val Lys Asn Thr  
 50 55 60

Gly Ser Ala Pro Val Asp Gly Trp Thr Leu Thr Phe Ser Phe Pro Ser  
 65 70 75 80

Gly Gln Gln Val Thr Gln Ala Trp Ser Ser Thr Val Thr Gln Ser Gly  
 85 90 95

Ser Ala Val Thr Val Arg Asn Ala Pro Trp Asn Gly Asn Ile Pro Ala  
 100 105 110

Gly Gly Thr Ala Gln Phe Gly Phe Gln Gly Ser His Thr Gly Thr Asn  
 115 120 125

Ala Ala Pro Thr Ala Phe Ser Leu Asn Gly Ala Pro Cys Thr Val Gly  
 130 135 140

Pro Thr Thr Ser Pro Thr Thr Arg Lys Leu Cys Ser Leu Asp Asn Gly  
 145 150 155 160

Asp Cys Asp Gln Phe Cys His Glu Glu Gln Asn Ser Val Val Cys Ser  
 165 170 175

Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn Gly Lys Ala Cys Ile Pro  
 180 185 190

Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr Leu Glu Arg Arg Lys Arg  
 195 200 205  
 Ser Val Ala Gln Ala Thr Ser Ser Ser Gly Glu Ala Pro Asp Ser Ile  
 210 215 220  
 Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu Asp Pro Thr Glu Asn Pro  
 225 230 235 240  
 Phe Asp Leu Leu Asp Phe Asp Gln Thr Gln Pro Glu Arg Gly Asp Asn  
 245 250 255  
 Asn Ile Glu Gly Arg Ile Val Gly Gly Gln Glu Cys Lys Asp Gly Glu  
 260 265 270  
 Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu Asn Glu Gly Phe Cys  
 275 280 285  
 Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu Thr Ala Ala His Cys  
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 Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val Gly Asp Arg Asn Thr  
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 Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu Val Glu Val Val Ile  
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 Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp Phe Asp Ile Ala Val  
 340 345 350  
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 355 360 365  
 Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr Leu Met Thr Gln Lys  
 370 375 380  
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 385 390 395 400  
 Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr Val Asp Arg Asn Ser  
 405 410 415  
 Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln Asn Met Phe Cys Ala  
 420 425 430  
 Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln Gly Asp Ser Gly Gly  
 435 440 445  
 Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe Val Thr Gly Ile Val  
 450 455 460  
 Ser Trp Gly Glu Gly Cys Ala Arg Lys Gly Lys Tyr Gly Ile Tyr Thr  
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 Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg Ser Met Lys Thr Arg

485

490

495

Gly Leu Pro Lys Ala Lys Pro Thr Ser His Asp Glu Leu  
 500 505

&lt;210&gt; 19

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Single strand DNA oligonucleotide

&lt;400&gt; 19

aaaagacgtc ggctagcgga ataatggtag cg

32

&lt;210&gt; 20

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Single strand DNA oligonucleotide

&lt;400&gt; 20

aaaaacgcgt tggggatggg gtcggac

27

&lt;210&gt; 21

&lt;211&gt; 1860

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; pBS-Sig-Tma-Fx-HDEL fusion construst

&lt;400&gt; 21

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taagacgtcg gctagcggaa taatggtagc gacagcaaaa tacggaacac cggatcatcga 180

tggagagata gacgagatct ggaacacgac agaggagata gagacgaaa cgggtggccat 240

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caagtggatc gacaggtcca tgaaaaccag gggcttgccc aaggccaagc ctactagtca 1800
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<210> 22

<211> 597

<212> PRT

<213> Artificial sequence

<220>

<223> pBS-Sig-Tma-Fx-HDEL fusion encoded product

<400> 22

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Met Ala Arg Lys Ser Leu Ile Phe Pro Val Ile Leu Leu Ala Val Leu
1           5           10          15

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Leu Phe Ser Pro Pro Ile Tyr Ser Ala Gly His Asp Tyr Arg Asp Ala
20          25          30

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Leu Arg Lys Thr Ser Ala Ser Gly Ile Met Val Ala Thr Ala Lys Tyr

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Glu Glu Ile Glu Thr Lys	Ala Val Ala Met Gly Ser	Leu Asp Lys Asn		
65	70	75	80	
Ala Thr Ala Lys Val Arg	Val Leu Trp Asp Glu Asn	Tyr Leu Tyr Val		
	85	90	95	
Leu Ala Ile Val Lys Asp	Pro Val Leu Asn Lys Asp	Asn Ser Asn Pro		
	100	105	110	
Trp Glu Gln Asp Ser Val	Glu Ile Phe Ile Asp Glu	Asn Asn His Lys		
	115	120	125	
Thr Gly Tyr Tyr Glu Asp	Asp Asp Ala Gln Phe Arg	Val Asn Tyr Met		
	130	135	140	
Asn Glu Gln Thr Phe Gly	Thr Gly Gly Ser Pro Ala	Arg Phe Lys Thr		
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Ala Val Lys Leu Ile Glu	Gly Gly Tyr Ile Val Glu	Ala Ala Ile Lys		
	165	170	175	
Trp Lys Thr Ile Lys Pro	Thr Pro Asn Thr Val Ile	Gly Phe Asn Ile		
	180	185	190	
Gln Val Asn Asp Ala Asn	Glu Lys Gly Gln Arg Val	Gly Ile Ile Ser		
	195	200	205	
Trp Ser Asp Pro Thr Asn	Asn Ser Trp Arg Asp Pro	Ser Lys Phe Gly		
	210	215	220	
Asn Leu Arg Leu Ile Lys	Gly Ser Gly Pro Thr Pro	Ser Pro Thr Arg		
	225	230	235	240
Lys Leu Cys Ser Leu Asp	Asn Gly Asp Cys Asp Gln	Phe Cys His Glu		
	245	250	255	
Glu Gln Asn Ser Val Val	Cys Ser Cys Ala Arg Gly	Tyr Thr Leu Ala		
	260	265	270	
Asp Asn Gly Lys Ala Cys	Ile Pro Thr Gly Pro Tyr	Pro Cys Gly Lys		
	275	280	285	
Gln Thr Leu Glu Arg Arg	Lys Arg Ser Val Ala Gln	Ala Thr Ser Ser		
	290	295	300	
Ser Gly Glu Ala Pro Asp	Ser Ile Thr Trp Lys Pro	Tyr Asp Ala Ala		
	305	310	315	320
Asp Leu Asp Pro Thr Glu	Asn Pro Phe Asp Leu	Leu Asp Phe Asp	Gln	
	325	330	335	

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 Asn Glu Glu Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe  
 370 375 380  
 Tyr Ile Leu Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys  
 385 390 395 400  
 Val Arg Val Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala  
 405 410 415  
 Val His Glu Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu  
 420 425 430  
 Thr Tyr Asp Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr  
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 450 455 460  
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 465 470 475 480  
 Arg Thr His Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu  
 485 490 495  
 Val Pro Tyr Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile  
 500 505 510  
 Ile Thr Gln Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp  
 515 520 525  
 Ala Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp  
 530 535 540  
 Thr Tyr Phe Val Thr Gly Ile Val Ser Trp Gly Glu Gly Cys Ala Arg  
 545 550 555 560  
 Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp  
 565 570 575  
 Ile Asp Arg Ser Met Lys Thr Arg Gly Leu Pro Lys Ala Lys Pro Thr  
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 Ser His Asp Glu Leu  
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